



IFWO

RAW SEQUENCE LISTING

DATE: 09/01/2004

PATENT APPLICATION: US/10/804,457

TIME: 12:51:43

Input Set : N:\Crif3\RULE60\10804457.raw

Output Set : N:\CRF4\09012004\J804457.raw

1 <110> APPLICANT: Friddle, Carl Johan
 2 Hilbun, Erin
 3 <120> TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the
 4 Same
 5 <130> FILE REFERENCE: LEX-0219-USA
 6 <140> CURRENT APPLICATION NUMBER: US/10/804,457
 7 <141> CURRENT FILING DATE: 2004-03-19.
 8 <150> PRIOR APPLICATION NUMBER: US/10/217,774
 9 <151> PRIOR FILING DATE: 2002-08-12
 10 <150> PRIOR APPLICATION NUMBER: US/09/930,872
 11 <151> PRIOR FILING DATE: 2001-08-14
 12 <150> PRIOR APPLICATION NUMBER: US 60/225,852
 13 <151> PRIOR FILING DATE: 2000-08-16
 14 <160> NUMBER OF SEQ ID NOS: 5
 15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1476
 19 <212> TYPE: DNA
 20 <213> ORGANISM: homo sapiens
 21 <400> SEQUENCE: 1

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23	gtggccgagc	aggcacctgc	gtgcgccatg	ggaccccgag	cggcagcgcc	tgggagcccc	120
24	agcgtcccg	gtcctcctcc	acccgcggag	cggccgggct	ggatggaaaa	gggcgaatat	180
25	gacctggtct	ctgectacga	ggttgaccac	aggggcgatt	acgtgtccca	tgaaatcatg	240
26	caccatcagc	ggcggagaag	agcagtggcc	gtgtccgagg	ttgagtctct	tcaccttcgg	300
27	ctgaaaggct	ccaggcacga	cttccacgtg	gatctgagga	cttccagcag	cctagtggct	360
28	cctggcttta	ttgtgcagac	gttgggaaag	acaggcacta	agtctgtgca	gactttaccg	420
29	ccagaggact	tctgtttcta	tcaaggctct	ttgcgatcac	acagaaaactc	ctcagtggcc	480
30	ctttcaacct	gccaaggctt	gtcaggcatg	atacgaacag	aagaggcaga	ttacttccta	540
31	aggccacttc	cttcacacct	ctcatggaaa	ctcgccagag	ctgcccagg	cagctcgcca	600
32	tcccacgtac	tgtacaagag	atccacagag	ccccatgctc	ctggggccag	tgaggctctg	660
33	gtgacctcaa	ggacatggga	gctggcacat	caacccctgc	acagcagcga	ccttcgctctg	720
34	ggactgccac	aaaagcagca	tttctgtgga	agacgcaaga	aatacatgcc	ccagcctccc	780
35	aaggaagacc	tcttcatctt	gccagatgag	tataagtctt	gcttacggca	taagcgctct	840
36	cttctgaggt	cccatagaaa	tgaagaactg	aacgtggaga	ccttggtggt	ggtcgacaaa	900
37	aagatgatgc	aaaacctatg	ccatgaaaat	atcaccacct	acgtgctcac	gatactcaac	960
38	atggtatctg	ctttattcaa	agatggaaca	ataggaggaa	acatcaacat	tgcaattgta	1020
39	ggtctgattc	ttctagaaga	tgaacagcca	ggactggtga	taagtcacca	cgcagaccac	1080
40	accttaagta	gcttctgcca	gtggcagctc	ggattgatgg	ggaaagatgg	gactcgctcat	1140
41	gaccacgcca	tcttactgac	tggctctggat	atatgttctt	ggaagaatga	gccctgtgac	1200
42	actttgggat	ttgcacccat	aagtgggaatg	tgtagtaaata	atcgagctg	cacgattaat	1260
43	gaagatacag	gtcttgagct	ggccttcacc	attgcccattg	agctctggaca	caactttggc	1320
44	atgattcatg	atggagaagg	gaacatgtgt	aaaaagtcgg	agggaacat	catgtcccct	1380

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45      acattggcag gacgcaatgg agtcttctcc tggtcaccct gcagccgcca gtatctacac      1440
46      aaatttctaa gatcagtga aatgccagct ctctga      1476
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50 <212> TYPE: PRT
51 <213> ORGANISM: homo sapiens
52 <400> SEQUENCE: 2
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55      Leu Leu Ala Gln Val Ala Glu Gln Ala Pro Ala Cys Ala Met Gly Pro
56      20          25          30
57      Ala Ala Ala Ala Pro Gly Ser Pro Ser Val Pro Arg Pro Pro Pro Pro
58      35          40          45
59      Ala Glu Arg Pro Gly Trp Met Glu Lys Gly Glu Tyr Asp Leu Val Ser
60      50          55          60
61      Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser His Glu Ile Met
62      65          70          75          80
63      His His Gln Arg Arg Arg Ala Val Ala Val Ser Glu Val Glu Ser
64      85          90          95
65      Leu His Leu Arg Leu Lys Gly Ser Arg His Asp Phe His Val Asp Leu
66      100         105         110
67      Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile Val Gln Thr Leu
68      115         120         125
69      Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro Pro Glu Asp Phe
70      130         135         140
71      Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn Ser Ser Val Ala
72      145         150         155         160
73      Leu Ser Thr Cys Gln Gly Leu Ser Gly Met Ile Arg Thr Glu Glu Ala
74      165         170         175
75      Asp Tyr Phe Leu Arg Pro Leu Pro Ser His Leu Ser Trp Lys Leu Gly
76      180         185         190
77      Arg Ala Ala Gln Gly Ser Ser Pro Ser His Val Leu Tyr Lys Arg Ser
78      195         200         205
79      Thr Glu Pro His Ala Pro Gly Ala Ser Glu Val Leu Val Thr Ser Arg
80      210         215         220
81      Thr Trp Glu Leu Ala His Gln Pro Leu His Ser Ser Asp Leu Arg Leu
82      225         230         235         240
83      Gly Leu Pro Gln Lys Gln His Phe Cys Gly Arg Arg Lys Lys Tyr Met
84      245         250         255
85      Pro Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys
86      260         265         270
87      Ser Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu
88      275         280         285
89      Glu Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln
90      290         295         300
91      Asn His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn
92      305         310         315         320
93      Met Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn
94      325         330         335

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95   Ile Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu
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97   Val Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp
98           355                     360                     365
99   Gln Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile
100          370                     375                     380
101   Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp
102          385                     390                     395                     400
103   Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser
104           405                     410                     415
105   Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala
106           420                     425                     430
107   His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn
108           435                     440                     445
109   Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly
110          450                     455                     460
111   Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His
112          465                     470                     475                     480
113   Lys Phe Leu Arg Ser Val Lys Met Pro Ala Leu
114           485                     490

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116 <210> SEQ ID NO: 3

117 <211> LENGTH: 3675

118 <212> TYPE: DNA

119 <213> ORGANISM: homo sapiens

120 <400> SEQUENCE: 3

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121   atgaagcccc gcgcgcgcgcg atggcggggc ttggcgggcg tgtggatgct gctggcgcgag      60
122   gtggccgagc aggcacctgc gtgcgccatg ggacccgcag cggcagcgcc tgggagcccc      120
123   agcgtcccgc gtcctcctcc acccgcgagc cggccgggct ggatggaaaa gggcgaatat      180
124   gacctggtct ctgcctacga ggttgaccac agggggcgatt acgtgtccca tgaaatcatg      240
125   caccatcagc ggcggagaag agcagtggcc gtgtccgagg ttgagtctct tcaccttcgg      300
126   ctgaaaggct ccaggcacga cttccacgtg gatctgagga cttccagcag cctagtggct      360
127   cctggcttta ttgtgcagac gttgggaaag acaggcacta agtctgtgca gactttaccg      420
128   ccagaggact tctgtttcta tcaaggctct ttgcgatcac acagaaactc ctcagtggcc      480
129   ctttcaacct gccaaaggct gtcaggcatg atacgaacag aagaggcaga ttacttccta      540
130   aggccacttc cttcacacct ctcatggaaa ctcggcagag ctgcccaggc cagctcgcca      600
131   tcccacgtac tgtacaagag atccacagag ccccatgctc ctggggccag tgaggctctg      660
132   gtgacctcaa ggacatggga gctggcacat caaccctgc acagcagcga ctttcgctg      720
133   ggactgccac aaaagcagca tttctgtgga agacgcaaga aatacatgcc ccagcctccc      780
134   aaggaagacc tcttcatctt gccagatgag tataagtctt gcttacggca taagcgctct      840
135   cttctgaggt cccatagaaa tgaagaactg aacgtggaga ccttggtggt ggtcgacaaa      900
136   aagatgatgc aaaacctatg ccatgaaaat atcaccacct acgtgctcac gataactaac      960
137   atggtatctg ctttattcaa agatggaaca ataggaggaa acatcaacat tgcaattgta     1020
138   ggtctgattc ttctagaaga tgaacagcca ggactggtga taagtcacca cgcagaccac     1080
139   accttaagta gtttctgcca gtggcagtct ggattgatgg ggaaagatgg gactcgctcat     1140
140   gaccacgcca tcttactgac tggctctggat atatgttctt ggaagaatga gccctgtgac     1200
141   actttgggat ttgcacccat aagtggaatg tgtagtaaat atcgcagctg cagattaat     1260
142   gaagatacag gtcttggaact ggcccttacc attgcccatt agtctggaca caactttggc     1320
143   atgattcatg atggagaagg gaacatgtgt aaaaagtcgg agggcaacat catgtcccct     1380
144   acattggcag gacgcaatgg agtcttctcc tggtcacctc gcagccgcca gtatctacac     1440

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145 aaattttctaa gcaccgctca agctatctgc cttgctgac agccaaagcc tgtgaaggaa 1500
146 tacaagtatc ctgagaaatt gccaggagaa ttatatgatg caaacacaca gtgcaagtgg 1560
147 cagttcggag agaaaagccaa gctctgcatg ctggacttta aaaaggacat ctgtaaagcc 1620
148 ctgtggtgcc atcggtattg aaggaaatgt gagactaaat ttatgccagc agcagaagcc 1680
149 acaattttgtg ggcatgacat gtggtgcccgg ggaggacagt gtgtgaaata tggatgatgaa 1740
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151 acctgctggag ggggagtatc tcataggagt cgcctctgca ccaaccccaa gccatcgcat 1860
152 ggagggaagt tctgtgaggg ctccactcgc actctgaagc tctgcaacag tcagaaatgt 1920
153 ccccgggaca gtgttgactt ccgtgctgct cagtgtgccg agcacaacag cagacgattc 1980
154 agaggcgccg actacaagtg gaagccttac actcaagtag aagatcagga cttatgcaaa 2040
155 ctctactgta tcgcagaagg atttgatttc ttcttttctt tgtcaaataa agtcaaagat 2100
156 gggactccat gctcggagga tagccgtaat gtttgtatag atgggatatg tgagagagtt 2160
157 ggatgtgaca atgtccttgg atctgatgct gttgaagacg tctgtggggg gtgtaacggg 2220
158 aataactcag cctgcacgat tcacaggggt ctctacacca agcaccacca caccaaccag 2280
159 tattatcaca tggtcaccat tcttctctga gcccgagta tccgcatcta tgaaatgaac 2340
160 gtctctacct cctacatttc tgtgcgcaat gccctcagaa ggtactacct gaatgggcac 2400
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162 tcctataatg agcccagaaa cttaatcgct actggaccaa ccaacgagac actgattgtg 2520
163 gagctgctgt ttccagggaag gaacccgggt gttgcctggg aatactccat gcctcgcttg 2580
164 gggaccgaga agcagccccc tgcccagccc agctacactt bggccatcgt gcgctctgag 2640
165 tgctccgtgt cctgcggagg gggacagatg accgtgagag agggctgcta cagagacctg 2700
166 aagtttcaag taaatatgtc cttctgcaat cccaagacac gacctgtcac ggggctgggtg 2760
167 ccttgcaaag tatctgcctg tctctccagc tggctcgtgg ggaactggag tgcttcagat 2820
168 cggacgtgtg gcggggggtg ccagagccgc cccgtgcagt gcacacggcg ggtgcactat 2880
169 gactcggagc cagtcccggc cagcctgtgc cctcagcctg ctccctccag caggcaggcc 2940
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171 acctgtggga aggggtggag gaagcgggca gtggcctgta agagcaccaa cccctcggcc 3060
172 agagcgcagc tgctgcccga cgtgtgtgc acctccgagc ccaagcccag gatgcatgaa 3120
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184 <210> SEQ ID NO: 4
185 <211> LENGTH: 1224
186 <212> TYPE: PRT
187 <213> ORGANISM: homo sapiens
188 <400> SEQUENCE: 4
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191 Leu Leu Ala Gln Val Ala Glu Gln Ala Pro Ala Cys Ala Met Gly Pro
192 20 25 30
193 Ala Ala Ala Ala Pro Gly Ser Pro Ser Val Pro Arg Pro Pro Pro
194 35 40 45

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195  Ala Glu Arg Pro Gly Trp Met Glu Lys Gly Glu Tyr Asp Leu Val Ser
196      50                      55                      60
197  Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser His Glu Ile Met
198  65                      70                      75                      80
199  His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser Glu Val Glu Ser
200                      85                      90                      95
201  Leu His Leu Arg Leu Lys Gly Ser Arg His Asp Phe His Val Asp Leu
202                      100                      105                      110
203  Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile Val Gln Thr Leu
204                      115                      120                      125
205  Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro Pro Glu Asp Phe
206                      130                      135                      140
207  Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn Ser Ser Val Ala
208  145                      150                      155                      160
209  Leu Ser Thr Cys Gln Gly Leu Ser Gly Met Ile Arg Thr Glu Glu Ala
210                      165                      170                      175
211  Asp Tyr Phe Leu Arg Pro Leu Pro Ser His Leu Ser Trp Lys Leu Gly
212                      180                      185                      190
213  Arg Ala Ala Gln Gly Ser Ser Pro Ser His Val Leu Tyr Lys Arg Ser
214                      195                      200                      205
215  Thr Glu Pro His Ala Pro Gly Ala Ser Glu Val Leu Val Thr Ser Arg
216                      210                      215                      220
217  Thr Trp Glu Leu Ala His Gln Pro Leu His Ser Ser Asp Leu Arg Leu
218  225                      230                      235                      240
219  Gly Leu Pro Gln Lys Gln His Phe Cys Gly Arg Arg Lys Lys Tyr Met
220                      245                      250                      255
221  Pro Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys
222                      260                      265                      270
223  Ser Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu
224                      275                      280                      285
225  Glu Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln
226                      290                      295                      300
227  Asn His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn
228  305                      310                      315                      320
229  Met Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn
230                      325                      330                      335
231  Ile Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu
232                      340                      345                      350
233  Val Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp
234                      355                      360                      365
235  Gln Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile
236                      370                      375                      380
237  Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp
238  385                      390                      395                      400
239  Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser
240                      405                      410                      415
241  Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala
242                      420                      425                      430
243  His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn

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The rules require that a line not exceed 72 characters in length. This includes spaces.

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VERIFICATION SUMMARY

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Output Set: N:\CRF4\09012004\J804457.raw

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